> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                SEQUENCE LISTING
 2
 3    (1)    General Information
 4
 5           (i) APPLICANT: Ruvkun, Gary
 6                          Morris, Jason
 7                          Tissenbaum, Heidi
 8
 9           (ii) TITLE OF THE INVENTION: AGE-1 POLYPEPTIDES AND RELATED
10                    MOLECULES AND METHODS
11
12           (iii) NUMBER OF SEQUENCES: 14
13
14           (iv) CORRESPONDENCE ADDRESS:
15              (A) ADDRESSEE: Clark & Elbing LLP
16              (B) STREET: 176 Federal Street
17              (C) CITY: Boston
18              (D) STATE: MA
19              (E) COUNTRY: USA
20              (F) ZIP: 02110
21
22           (v) COMPUTER READABLE FORM:
23              (A) MEDIUM TYPE: Diskette
24              (B) COMPUTER: IBM Compatible
25              (C) OPERATING SYSTEM: DOS
26              (D) SOFTWARE: FastSEQ for Windows Version 2.0
27
28           (vi) CURRENT APPLICATION DATA:
29              (A) APPLICATION NUMBER: US97/13914
30              (B) FILING DATE: 07-AUG-1997
31              (C) CLASSIFICATION:
32
33           (vii) PRIOR APPLICATION DATA:
34              (A) APPLICATION NUMBER: 60/023,382
35              (B) FILING DATE: 07-AUG-1996
36
37
38
39           (viii) ATTORNEY/AGENT INFORMATION:
40              (A) NAME: Elbing, Karen L
41              (B) REGISTRATION NUMBER: 35,238
42              (C) REFERENCE/DOCKET NUMBER: 08472/704WO2
43
44           (ix) TELECOMMUNICATION INFORMATION:
45              (A) TELEPHONE: 617-428-0200
46              (B) TELEFAX: 617-428-7045
```

--> line 29

Corrected Diskette Needed — Does Not Comply (handwritten annotation)

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/908,453*

INPUT SET: S29199.raw

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47            (C) TELEX:
48
49
50        (2) INFORMATION FOR SEQ ID NO:1:
51
52      (i) SEQUENCE CHARACTERISTICS:
53        (A) LENGTH: 1146 amino acids
54        (B) TYPE: amino acid
55        (C) STRANDEDNESS: unknown
56        (D) TOPOLOGY: linear
57
58      (ii) MOLECULE TYPE: protein
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62  Met His Val Asn Ile Leu His Pro Gln Leu Gln Thr Met Val Glu Gln
63   1           5               10               15
64  Trp Gln Met Arg Glu Arg Pro Ser Leu Glu Thr Glu Asn Gly Lys Gly
65           20              25              30
66  Ser Leu Leu Leu Glu Asn Glu Gly Val Ala Asp Ile Ile Thr Met Cys
67         35              40              45
68  Pro Phe Gly Glu Val Ile Ser Val Val Phe Pro Trp Phe Leu Ala Asn
69         50              55              60
70  Val Arg Thr Ser Leu Glu Ile Lys Leu Ser Asp Phe Lys His Gln Leu
71  65              70              75              80
72  Phe Glu Leu Ile Ala Pro Met Lys Trp Gly Thr Tyr Ser Val Lys Pro
73              85              90              95
74  Gln Asp Tyr Val Phe Arg Gln Leu Asn Asn Phe Gly Glu Ile Glu Val
75          100             105             110
76  Ile Phe Asn Asp Asp Gln Pro Leu Ser Lys Leu Glu Leu His Gly Thr
77          115             120             125
78  Phe Pro Met Leu Phe Leu Tyr Gln Pro Asp Gly Ile Asn Arg Asp Lys
79          130             135             140
80  Glu Leu Met Ser Asp Ile Ser His Cys Leu Gly Tyr Ser Leu Asp Lys
81  145             150             155             160
82  Leu Glu Glu Ser Leu Asp Glu Glu Leu Arg Gln Phe Arg Ala Ser Leu
83              165             170             175
84  Trp Ala Arg Thr Lys Lys Thr Cys Leu Thr Arg Gly Leu Glu Gly Thr
85              180             185             190
86  Ser His Tyr Ala Phe Pro Glu Glu Gln Tyr Leu Cys Val Gly Glu Ser
87          195             200             205
88  Cys Pro Lys Asp Leu Glu Ser Lys Val Lys Ala Ala Lys Leu Ser Tyr
89          210             215             220
90  Gln Met Phe Trp Arg Lys Arg Lys Ala Glu Ile Asn Gly Val Cys Glu
91  225             230             235             240
92  Lys Met Met Lys Ile Gln Ile Glu Phe Asn Pro Asn Glu Thr Pro Lys
93              245             250             255
94  Ser Leu Leu His Thr Phe Leu Tyr Glu Met Arg Lys Leu Asp Val Tyr
95          260             265             270
96  Asp Thr Asp Asp Pro Ala Asp Glu Gly Trp Phe Leu Gln Leu Ala Gly
97          275             280             285
98  Arg Thr Thr Phe Val Thr Asn Pro Asp Val Lys Leu Thr Ser Tyr Asp
99          290             295             300
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/908,453*

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100   Gly Val Arg Ser Glu Leu Glu Ser Tyr Arg Cys Pro Gly Phe Val Val
101   305               310               315           320
102   Arg Arg Gln Ser Leu Val Leu Lys Asp Tyr Cys Arg Pro Lys Pro Leu
103               325               330               335
104   Tyr Glu Pro His Tyr Val Arg Ala His Glu Arg Lys Leu Ala Leu Asp
105           340               345               350
106   Val Leu Ser Val Ser Ile Asp Ser Thr Pro Lys Gln Ser Lys Asn Ser
107           355               360                 365
108   Asp Met Val Met Thr Asp Phe Arg Pro Thr Ala Ser Leu Lys Gln Val
109       370               375               380
110   Ser Leu Trp Asp Leu Asp Ala Asn Leu Met Ile Arg Pro Val Asn Ile
111   385               390               395               400
112   Ser Gly Phe Asp Phe Pro Ala Asp Val Asp Met Tyr Val Arg Ile Glu
113               405               410               415
114   Phe Ser Val Tyr Val Gly Thr Leu Thr Leu Ala Ser Lys Ser Thr Thr
115           420               425               430
116   Lys Val Asn Ala Gln Phe Ala Lys Trp Asn Lys Glu Met Tyr Thr Phe
117           435               440               445
118   Asp Leu Tyr Met Lys Asp Met Pro Pro Ser Ala Val Leu Ser Ile Arg
119       450               455               460
120   Val Leu Tyr Gly Lys Val Lys Leu Lys Ser Glu Glu Phe Glu Val Gly
121   465               470               475               480
122   Trp Val Asn Met Ser Leu Thr Asp Trp Arg Asp Glu Leu Arg Gln Gly
123               485               490               495
124   Gln Phe Leu Phe His Leu Trp Ala Pro Glu Pro Thr Ala Asn Arg Ser
125           500               505               510
126   Arg Ile Gly Glu Asn Gly Ala Arg Ile Gly Thr Asn Ala Ala Val Thr
127       515               520               525
128   Ile Glu Ile Ser Ser Tyr Gly Gly Arg Val Arg Met Pro Ser Gln Gly
129       530               535               540
130   Gln Tyr Thr Tyr Leu Val Lys His Arg Ser Thr Trp Thr Glu Thr Leu
131   545               550               555               560
132   Asn Ile Met Gly Asp Asp Tyr Glu Ser Cys Ile Arg Asp Pro Gly Tyr
133               565               570               575
134   Lys Lys Leu Gln Met Leu Val Lys Lys His Glu Ser Gly Ile Val Leu
135               580               585               590
136   Glu Glu Asp Glu Gln Arg His Val Trp Met Trp Arg Arg Tyr Ile Gln
137           595               600               605
138   Lys Gln Glu Pro Asp Leu Leu Ile Val Leu Ser Glu Leu Ala Phe Val
139           610               615               620
140   Trp Thr Asp Arg Glu Asn Phe Ser Glu Leu Tyr Val Met Leu Glu Lys
141   625               630               635               640
142   Trp Lys Pro Pro Ser Val Ala Ala Ala Leu Thr Leu Leu Gly Lys Arg
143               645               650               655
144   Cys Thr Asp Arg Val Ile Arg Lys Phe Ala Val Glu Lys Leu Asn Glu
145           660               665               670
146   Gln Leu Ser Pro Val Thr Phe His Leu Phe Ile Leu Pro Leu Ile Gln
147           675               680               685
148   Ala Leu Lys Tyr Glu Pro Arg Ala Gln Ser Glu Val Gly Met Met Leu
149       690               695               700
150   Leu Thr Arg Ala Leu Cys Asp Tyr Arg Ile Gly His Arg Leu Phe Trp
151   705               710               715               720
152   Leu Leu Arg Ala Glu Ile Ala Arg Leu Arg Asp Cys Asp Leu Lys Ser
```

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153                    725                    730                    735
154   Glu Glu Tyr Arg Arg Ile Ser Leu Leu Met Glu Ala Tyr Leu Arg Gly
155                    740                    745                    750
156   Asn Glu Glu His Ile Lys Ile Ile Thr Arg Gln Val Asp Met Val Asp
157                    755                    760                    765
158   Glu Leu Thr Arg Ile Ser Thr Leu Val Lys Gly Met Pro Lys Asp Val
159                    770                    775                    780
160   Ala Thr Met Lys Leu Arg Asp Glu Leu Arg Ser Ile Ser His Lys Met
161   785                    790                    795                    800
162   Glu Asn Met Asp Ser Pro Leu Asp Pro Val Tyr Lys Leu Gly Glu Met
163                    805                    810                    815
164   Ile Ile Asp Lys Ala Ile Val Leu Gly Ser Ala Lys Arg Pro Leu Met
165                    820                    825                    830
166   Leu His Trp Lys Asn Lys Asn Pro Lys Ser Asp Leu His Leu Pro Phe
167                    835                    840                    845
168   Cys Ala Met Ile Phe Lys Asn Gly Asp Asp Leu Arg Gln Asp Met Leu
169                    850                    855                    860
170   Val Leu Gln Val Leu Glu Val Met Asp Asn Ile Trp Lys Ala Ala Asn
171   865                    870                    875                    880
172   Ile Asp Cys Cys Leu Asn Pro Tyr Ala Val Leu Pro Met Gly Glu Met
173                    885                    890                    895
174   Ile Gly Ile Ile Glu Val Val Pro Asn Cys Lys Thr Ile Phe Glu Ile
175                    900                    905                    910
176   Gln Val Gly Thr Gly Phe Met Asn Thr Ala Val Arg Ser Ile Asp Pro
177                    915                    920                    925
178   Ser Phe Met Asn Lys Trp Ile Arg Lys Gln Cys Gly Ile Glu Asp Glu
179                    930                    935                    940
180   Lys Lys Lys Ser Lys Lys Asp Ser Thr Lys Asn Pro Ile Glu Lys Lys
181   945                    950                    955                    960
182   Ile Asp Asn Thr Gln Ala Met Lys Lys Tyr Phe Glu Ser Val Asp Arg
183                    965                    970                    975
184   Phe Leu Tyr Ser Cys Val Gly Tyr Ser Val Ala Thr Tyr Ile Met Gly
185                    980                    985                    990
186   Ile Lys Asp Arg His Ser Asp Asn Leu Met Leu Thr Glu Asp Gly Lys
187                    995                    1000                    1005
188   Tyr Val His Ile Asp Phe Gly His Ile Leu Gly His Gly Lys Thr Lys
189                    1010                    1015                    1020
190   Leu Gly Ile Gln Arg Asp Arg Gln Pro Phe Ile Leu Thr Glu His Phe
191   025                    1030                    1035                    1040
192   Met Thr Val Ile Arg Ser Gly Lys Ser Val Asp Gly Asn Ser His Glu
193                    1045                    1050                    1055
194   Leu Gln Lys Phe Lys Thr Leu Cys Val Glu Ala Tyr Glu Val Met Trp
195                    1060                    1065                    1070
196   Asn Asn Arg Asp Leu Phe Val Ser Leu Phe Thr Leu Met Leu Gly Met
197                    1075                    1080                    1085
198   Glu Leu Pro Glu Leu Ser Thr Lys Ala Asp Leu Asp His Leu Lys Lys
199                    1090                    1095                    1100
200   Thr Leu Phe Cys Asn Gly Glu Ser Lys Glu Glu Ala Arg Lys Phe Phe
201   105                    1110                    1115                    1120
202   Ala Gly Ile Tyr Glu Glu Ala Phe Asn Gly Ser Trp Ser Thr Lys Thr
203                    1125                    1130                    1135
204   Asn Trp Leu Phe His Ala Val Lys His Tyr
205                    1140                    1145
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/908,453*

INPUT SET: S29199.raw

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206
207              (2) INFORMATION FOR SEQ ID NO:2:
208
209          (i) SEQUENCE CHARACTERISTICS:
210             (A) LENGTH: 3504 base pairs
211             (B) TYPE: nucleic acid
212             (C) STRANDEDNESS: double
213             (D) TOPOLOGY: linear
214
215         (ii) MOLECULE TYPE: cDNA
216
217         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
218
219    CGGAAGCCAT GGAGCTCGAG ATCTGATTGC TGGACACGGA CGGAACTCCG ACGTATCTCG      60
220    CAGATGCATG TTAACATTTT ACATCCACAA CTGCAAACGA TGGTCGAGCA GTGGCAAATG     120
221    CGAGAACGCC CATCGCTGGA GACCGAGAAT GGCAAAGGAT CGCTGCTCCT GGAAAATGAA     180
222    GGTGTCGCAG ATATCATCAC TATGTGTCCA TTCGGAGAAG TTATTAGTGT AGTATTTCCG     240
223    TGGTTTCTTG CAAATGTGCG AACATCGCTA GAAATCAAGC TATCAGATTT CAAACATCAA     300
224    CTTTTCGAAT TGATTGCTCC GATGAAGTGG GGAACATATT CCGTAAAGCC ACAGGATTAT     360
225    GTGTTCAGAC AGTTGAATAA TTTCGGCGAA ATTGAAGTTA TATTTAACGA CGATCAACCC     420
226    CTGTCGAAAT TAGAGCTCCA CGGCACTTTC CCAATGCTTT TTCTCTACCA ACCTGATGGA     480
227    ATAAACAGGG ATAAAGAATT AATGAGTGAT ATAAGTCATT GTCTAGGATA CTCACTGGAT     540
228    AAACTGGAAG AGAGCCTCGA TGAGGAACTC CGTCAATTTC GTGCTTCTCT CTGGGCTCGT     600
229    ACGAAGAAAA CGTGCTTGAC ACGTGGACTT GAGGGTACCA GTCACTACGC GTTCCCCGAA     660
230    GAACAGTACT TGTGTGTTGG TGAATCGTGC CCGAAAGATT TGGAATCAAA AGTCAAGGCT     720
231    GCCAAGCTGA GTTATCAGAT GTTTTGGAGA AAACGTAAAG CGGAAATCAA TGGAGTTTGC     780
232    GAGAAAATGA TGAAGATTCA AATTGAATTC AATCCGAACG AAACTCCGAA ATCTCTGCTT     840
233    CACACGTTTC TCTACGAAAT GCGAAAATTG GATGTATACG ATACCGATGA TCCTGCAGAT     900
234    GAAGGATGGT TTCTTCAATT GGCTGGACGT ACCACGTTTG TTACAAATCC AGATGTCAAA     960
235    CTTACGTCTT ATGATGGTGT CCGTTCGGAA CTGGAAAGCT ATCGATGCCC TGGATTCGTT    1020
236    GTTCGCCGAC AATCACTAGT CCTCAAAGAC TATTGTCGCC CAAAACCACT CTACGAACCA    1080
237    CATTATGTGA GAGCACACGA ACGAAAACTT GCTCTAGACG TGCTCAGCGT GTCTATAGAT    1140
238    AGCACACCAA AACAGAGCAA GAACAGTGAC ATGGTTATGA CTGATTTTCG TCCGACAGCT    1200
239    TCACTCAAAC AAGTTTCACT TTGGGACCTT GACGCGAATC TTATGATACG GCCTGTGAAT    1260
240    ATTTCTGGAT TCGATTTCCC GGCCGACGTG GATATGTACG TTCGAATCGA ATTCAGTGTA    1320
241    TATGTGGGGA CACTGACGCT GGCATCAAAA TCTACAACAA AAGTGAATGC TCAATTTGCA    1380
242    AAATGGAATA AGGAAATGTA CACTTTTGAT CTATACATGA AGGATATGCC ACCATCTGCA    1440
243    GTACTCAGCA TTCGTGTTTT GTACGGAAAA GTGAAATTAA AAAGTGAAGA ATTCGAAGTT    1500
244    GGTTGGGTAA ATATGTCCCT AACCGATTGG AGAGATGAAC TACGACAAGG ACAATTTTTA    1560
245    TTCCATCTGT GGGCTCCTGA ACCGACTGCC AATCGTAGTA GGATCGGAGA AAATGGAGCA    1620
246    AGGATAGGCA CCAACGCAGC GGTTACAATT GAAATCTCAA GTTATGGTGG TAGAGTTCGA    1680
247    ATGCCGAGTC AAGGACAATA CACATATCTC GTCAAGCACC GAAGTACTTG GACGGAAACT    1740
248    TTGAATATTA TGGGTGATGA CTATGAGTCG TGTATCAGAG ATCCAGGATA TAAGAAGCTT    1800
249    CAGATGCTTG TCAAGAAGCA TGAATCTGGA ATTGTATTAG AGGAAGATGA ACAACGTCAT    1860
250    GTCTGGATGT GGAGGAGATA CATTCAAAAG CAGGAGCCTG ATTTGCTCAT TGTGCTCTCC    1920
251    GAACTCGCAT TTGTGTGGAC TGATCGTGAG AACTTTTCCG AGCTCTATGT GATGCTTGAA    1980
252    AAATGGAAAC CGCCGAGTGT GGCAGCCGCG TTGACTTTGC TTGGAAAACG TTGCACGGAT    2040
253    CGTGTGATTC GAAAGTTTGC AGTGGAGAAG TTGAATGAGC AGCTGAGCCC GGTCACATTC    2100
254    CATCTTTTCA TATTGCCTCT CATACAGGCG TTGAAGTACG AACCGCGTGC TCAATCGGAA    2160
255    GTTGGAATGA TGCTCTTGAC TAGAGCTCTC TGCGATTATC GAATTGGACA TCGACTTTTC    2220
256    TGGCTGCTCC GTGCAGAGAT TGCTCGTTTG AGAGATTGTG ATCTGAAAAG TGAAGAATAT    2280
257    CGCCGTATCT CACTTCTGAT GGAAGCTTAC CTCCGTGGAA ATGAAGAGCA CATCAAGATC    2340
258    ATCACCCGAC AAGTTGACAT GGTTGATGAG CTCACACGAA TCAGCACTCT TGTCAAAGGA    2400
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/908,453*

INPUT SET: S29199.raw

Line	Error	Original Text
29	Wrong application Serial Number	(A) APPLICATION NUMBER: US97/13914